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PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants : Nobuyuki Itoh et al.  
Application No. : 09/801,968  
Filed : March 7, 2001  
For : HUMAN FGF-23 GENE AND GENE EXPRESSION PRODUCTS

Examiner :  
Art Unit : 1646  
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Date : July 2, 2001

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FILING FORMAL DRAWINGS

Commissioner for Patents:

Enclosed are 22 sheets of formal drawings, Figures 1-16, for filing in the above-identified application.

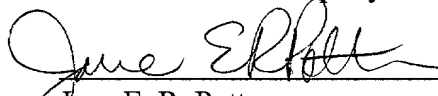


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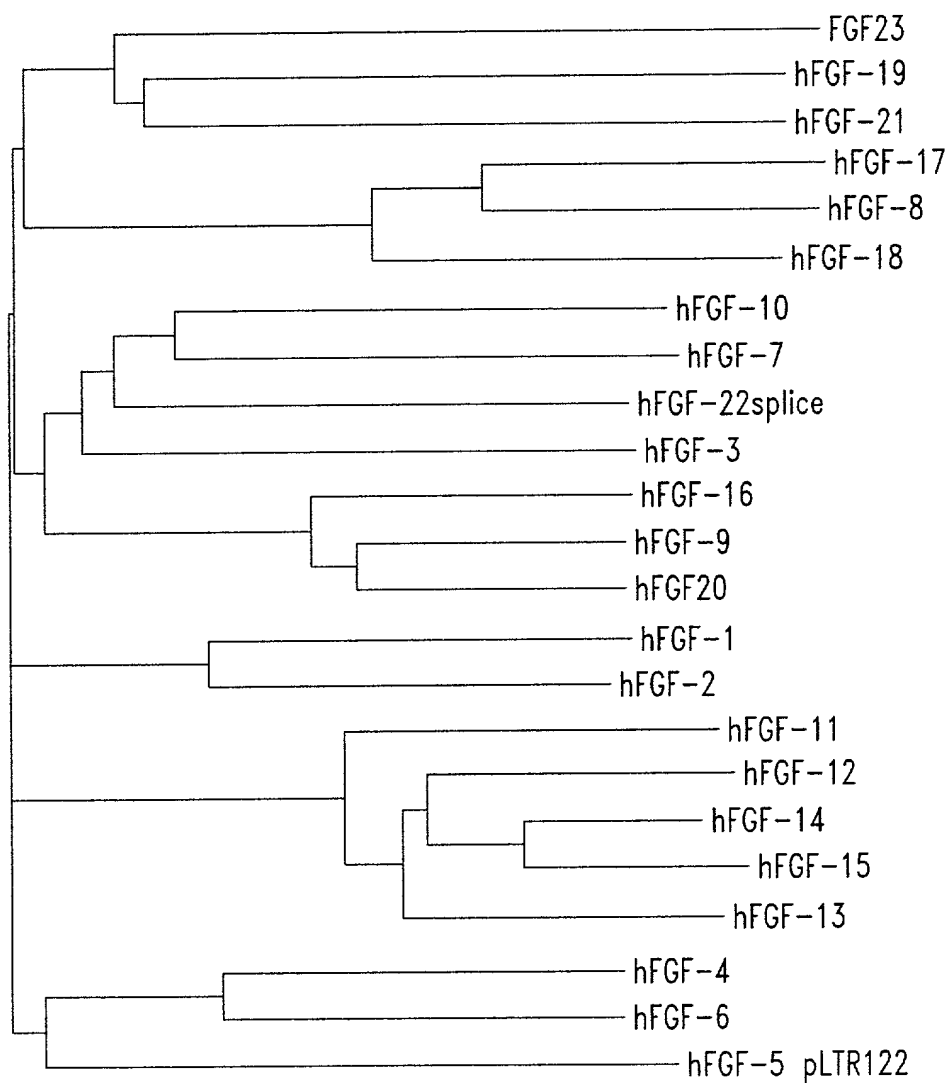
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Respectfully submitted,

Seed Intellectual Property Law Group PLLC

  
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(JEP:cew) #191149

*Fig. 1*

Mouse FGF-23

10 20 30 40 50 60  
ATGCTAGGGACCTGCCTTAGACTCCTGGTGGGCGTGCTCTGCACTGTCTGCAGCTTGGGC  
M L G T C L R L L V G V L C T V C S L G

70 80 90 100 110 120  
ACTGCTAGAGCCTATCCAGACACTTCCCCATTGCTTGGCTCCAACTGGGGAAGCCTGACC  
T A R A Y P D T S P L L G S N W G S L T

130 140 150 160 170 180  
CACCTGTACACGGCTACAGCCAGGACCAGCTATCACCTACAGATCCATAGGGATGGTCAT  
H L Y T A T A R T S Y H L Q I H R D G H

190 200 210 220 230 240  
GTAGATGGCACCCCCATCAGACCATCTACAGTGCCCTGATGATTACATCAGAGGACGCC  
V D G T P H Q T I Y S A L M I T S E D A

250 260 270 280 290 300  
GGCTCTGTGGTGATAACAGGAGCCATGACTCGAAGGTTCTTTGTATGGATCTCCACGGC  
G S V V I T G A M T R R F L C M D L H G

310 320 330 340 350 360  
AACATTTTTGGATCGCTTCACTTCAGCCCAGAGAATTGCAAGTTCCGCCAGTGACGCTG  
N I F G S L H F S P E N C K F R Q W T L

370 380 390 400 410 420  
GAGAATGGCTATGACGTCTACTTGTGCGAGAAGCATCACTACCTGGTGAGCCTGGGCCGC  
E N G Y D V Y L S Q K H H Y L V S L G R

430 440 450 460 470 480  
GCCAAGCGCATTTTCCAGCCGGGCACCAACCCGCCGCCCTTCTCCAGTTCTGGCTCGC  
A K R I F Q P G T N P P P F S Q F L A R

490 500 510 520 530 540  
AGGAACGAGGTCCCGTGCTGCACTTCTACACTGTTGCGCCACGGCGCCACACGCGCAGC  
R N E V P L L H F Y T V R P R R H T R S

550 560 570 580 590 600  
GCCGAGGACCCACCCGAGCGCGACCACTGAACGTGCTCAAGCCGCGGCCCCGCGCCACG  
A E D P P E R D P L N V L K P R P R A T

*Fig. 2A*

550 560 570 580 590 600  
GCCGAGGACCCACCCGAGCGCGACCCACTGAACGTGCTCAAGCCGCGGCCCCGCGCCACG  
A E D P P E R D P L N V L K P R P R A T

610 620 630 640 650 660  
CCTGTGCCTGTATCCTGCTCTCGCGAGCTGCCGAGCGCAGAGGAAGGTGGCCCCGCGAGCC  
P V P V S C S R E L P S A E E G G P A A

670 680 690 700 710 720  
AGCGATCCTCTGGGGGTGCTGCGCAGAGGCCGTGGAGATGCTCGCGGGGGCGCGGGAGGC  
S D P L G V L R R G R G D A R G G A G G

730 740 750 760  
GCGGATAGGTGTCGCCCCTTTCCAGGTTTCGTCTAG  
A D R C R P F P R F V \*

*Fig. 2B*

## Human FGF-23

10 20 30 40 50 60  
atgttgggggcccgccctcaggctctgggtctgtgccttgtgcagcgtctgcagcatgagc  
M L G A R L R L W V C A L C S V C S M S

70 80 90 100 110 120  
gtcctcagagcctatcccaatgcctccccactgctcggctccagctggggtggcctgac  
V L R A Y P N A S P L L G S S W G G L I

130 140 150 160 170 180  
cacctgtacacagccacagccaggaacagctaccacctgcagatccacaagaatggccat  
H L Y T A T A R N S Y H L Q I H K N G H

190 200 210 220 230 240  
gtggatggcgcaccccatcagaccatctacagtgccttgatgatcagatcagaggatgct  
V D G A P H Q T I Y S A L M I R S E D A

250 260 270 280 290 300  
ggctttgtggtgattacaggtgtgatgagcagaagatacctctgcatggatttcagaggc  
G F V V I T G V M S R R Y L C M D F R G

310 320 330 340 350 360  
aacatttttgatcacactatttcgacccggagaactgcaggttccaacaccagacgctg  
N I F G S H Y F D P E N C R F Q H Q T L

370 380 390 400 410 420  
gaaaacgggtacgacgtctaccactctcctcagtatcacttcttggtcagtctgggccgg  
E N G Y D V Y H S P Q Y H F L V S L G R

430 440 450 460 470 480  
gcgaagagagccttcctgccaggcatgaacccacccccgtactcccagttcctgtcccgg  
A K R A F L P G M N P P P Y S Q F L S R

490 500 510 520 530 540  
aggaacgagatccccctaattcacttcaacacccccataccacggcggcacacccggagc  
R N E I P L I H F N T P I P R R H T R S

550 560 570 580 590 600  
gccgaggacgactcggagcgggacccccctgaacgtgctgaagccccgggcccggatgacc  
A E D D S E R D P L N V L K P R A R M T

*Fig. 3A*

610 620 630 640 650 660  
ccggccccggcctcctgttcacaggagctcccgagcgccgaggacaacagcccgatggcc  
P A P A S C S Q E L P S A E D N S P M A

670 680 690 700 710 720  
agtgaccattaggggtgggtcaggggcgggtcgagtgaacacgcacgctgggggaacgggc  
S D P L G V V R G G R V N T H A G G T G

730 740 750 760  
ccggaaggctgccgccccttcgccaagttcatctag  
P E G C R P F A K F I \*

*Fig. 3B*

FIG. 4

Mouse FGF-23	MLGTCLRLLVGVLCTVCSLGTARAYPDTPLLSNWGSLTHLYTATARTSYHLQIHRDGH	60
	*** *	
Human FGF-23	MLGARLRLWVCALCSVMSVLRAYPNASPLLGSSWGGLIHLTYTARNSYHLQIHKNGH	60
	*** *	
	VDGTPHQTIYSALMITSEDAGSVVITGAMTRRFLCMDLHGNIFGSLHFSPEACKFRQWTL	120
	*** *	
	VDGAPHQTIYSALMIRSEDAGFVITGVMSRRYLCMDFRGNIFGSHYFDPENCRCFQHQL	120
	*** *	
	ENGVDVYLSQKHYYLVSLGRAKRIFQPGTNPFPFSQFLARRNEVPLLHFYTVRPRRHTRS	180
	***** *	
	ENGVDVYHSPQYHFLVSLGRAKRAFLPGMNPPYPYSQFLSRRNEIPLIHENTPIPRRHTRS	180
	***** *	
	AEDPPERDPLNVLKPRPRATPVVSCSRELPSAEEGGPAASDPLGVLRGRGDARGGAGG	240
	*** *	
	AEDDSERDPLNVLKPRARMTAPASCSELPSAEDNSPMASDPLGVVVRGGRVNTHAGGTG	240
	***** *	
	ADRCRPFPRFV 251	
	.. ***** *	
	PEGCRPFACFI 251	

Fig. 4

Human FGF-23	MLGARLRLLWVCALCSVCSMSVLRAYPNVASPLLLGSSWGG---L IHLVTATAR--NSYHL	53
	....* * . . . . . * * * * . ** . * **** . . . . . *	
Human FGF-19	MMSGCVVHVWITLAGLWLAVAGRPLAFSDAGPHVHYGWDPTIRLRHLYTSGPHGLSSCFL	60
	QIHKNGHVDGAPHQTIYSALMIRSEDAGFVITGVMSRRRYLCMDFRGNIFGSHYFDPENC	113
	* *	
	RIRADGVWDCARGQSAHSLLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDC	120
	RFQHQTLENGYDVYHSPQYHFLVSLGRAK-RAFLPGMNPYPYSQFLSRRNEIPLIHFNTP	172
	* ..... ** ** * * . . . . . ** * * * * * *	
	AFFFFIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMWPEEPEDLR	180
	I PRRHTRSAEDDSERDPLNVLKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRV	232
	GHLESDMFSSPLETDSMDPFGLVTGLEAVRSPSFEK	216
	NTHAGGTGPEGCRPFKFI	251

Fig. 5



FIG. 6

Human FGF-23	MLGARLRRLWCALCS-VCSMSVLRAYPNASPLLG-SSWGGGLIHLYTATARNs-YH	52
	*** * . . . . * . . . . * . . . . *	
Human FGF-21	MDSDETGFEHSGLWVSLAGLLGACQAHPIPDSSPLLQFGGQVRQRYLYTDDAQQTEAH	60
	LQIHKNHVDGAPHQTIYSALMIRSEDAGFVWITGVMSRRYLCMDFRGNIFGSHYFDPEN	112
	* *	
	LEIREDTVGGAADQSPESLLQLKALKPGVIQILGVKTSRFLCQRPDQALYGSLLHFDPEA	120
	CRFQHQTLENGYDVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRRNEIPLIHFNTP	172
	* *	
	CSFRELLLEDGYNVYQSEAHGLPLHLPGNKSP-HRDPAPRGPARFLPLPGLPPALP--EP	177
	IPRRHTRSAEDDSERDPLNLKPRARMTAPASCSELPSAEDNSPMASDPLGVVRGGRV	232
	* . . . * . . . . * . . . . *	
	-PGILAPQPPDVGSSDPLSMVGPSQGRSPSYAS	209
	NTHAGGTGPEGCRPFAKFI	251

Fig. 6

Codon usage for yeast (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	33.00	0.86	0.01
Gly	GGA	70.00	1.82	0.02
Gly	GGT	2672.00	69.62	0.91
Gly	GGC	171.00	4.46	0.06
Glu	GAG	277.00	7.22	0.10
Glu	GAA	2442.00	63.63	0.90
Asp	GAT	1100.00	28.66	0.48
Asp	GAC	1211.00	31.55	0.52
Val	GTG	117.00	3.05	0.04
Val	GTA	75.00	1.95	0.03
Val	GTT	1548.00	40.33	0.56
Val	GTC	1026.00	26.73	0.37
Ala	GCG	36.00	0.94	0.01
Ala	GCA	203.00	5.29	0.06
Ala	GCT	2221.00	57.87	0.65
Ala	GCC	969.00	25.25	0.28
Arg	AGG	20.00	0.52	0.01
Arg	AGA	1336.00	34.81	0.83
Ser	AGT	116.00	3.02	0.05
Ser	AGC	94.00	2.45	0.04
Lys	AAG	2365.00	61.62	0.78
Lys	AAA	651.00	16.96	0.22
Asn	AAT	347.00	9.04	0.22
Asn	AAC	1259.00	32.80	0.78
Met	ATG	766.00	19.96	1.00
Ile	ATA	43.00	1.12	0.02
Ile	ATT	1223.00	31.87	0.52
Ile	ATC	1070.00	27.88	0.46
Thr	ACG	28.00	0.73	0.01
Thr	ACA	126.00	3.28	0.06

*Fig. 7A*

Thr	ACT	1129.00	29.42	0.50
Thr	ACC	962.00	25.07	0.43
Trp	TGG	325.00	8.47	1.00
End	TGA	10.00	0.26	0.09
Cys	TGT	254.00	6.62	0.89
Cys	TGC	33.00	0.86	0.11
End	TAG	11.00	0.29	0.10
End	TAA	85.00	2.21	0.80
Tyr	TAT	219.00	5.71	0.19
Tyr	TAC	913.00	23.79	0.81
Leu	TTG	2202.00	57.38	0.69
Leu	TTA	576.00	15.01	0.18
Phe	TTT	432.00	11.26	0.27
Phe	TTC	1145.00	29.83	0.73
Ser	TCG	26.00	0.68	0.01
Ser	TCA	149.00	3.88	0.06
Ser	TCT	1279.00	33.33	0.52
Ser	TCC	818.00	21.31	0.33
Arg	CGG	0.00	0.00	0.00
Arg	CGA	1.00	0.03	0.00
Arg	CGT	249.00	6.49	0.15
Arg	CGC	5.00	0.13	0.00
Gln	CAG	62.00	1.62	0.05
Gln	CAA	1225.00	31.92	0.95
His	CAT	236.00	6.15	0.35
His	CAC	433.00	11.28	0.65
Leu	CTG	52.00	1.35	0.02
Leu	CTA	236.00	6.15	0.07
Leu	CTT	90.00	2.35	0.03
Leu	CTC	14.00	0.36	0.00
Pro	CCG	10.00	0.26	0.01
Pro	CCA	1271.00	33.12	0.80
Pro	CCT	279.00	7.27	0.18
Pro	CCC	33.00	0.86	0.02

*Fig. 7B*

Codon usage for Drosophila (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	6.00	0.28	0.00
Gly	GGA	380.00	18.04	0.22
Gly	GGT	575.00	27.29	0.34
Gly	GGC	746.00	35.41	0.44
Glu	GAG	1217.00	57.77	0.91
Glu	GAA	115.00	5.46	0.09
Asp	GAT	503.00	23.88	0.43
Asp	GAC	654.00	31.04	0.57
Val	GTG	719.00	34.13	0.45
Val	GTA	29.00	1.38	0.02
Val	GTT	226.00	10.73	0.14
Val	GTC	608.00	28.86	0.38
Ala	GCG	94.00	4.46	0.05
Ala	GCA	80.00	3.80	0.04
Ala	GCT	446.00	21.17	0.24
Ala	GCC	1277.00	60.61	0.67
Arg	AGG	48.00	2.28	0.06
Arg	AGA	12.00	0.57	0.01
Ser	AGT	16.00	0.76	0.01
Ser	AGC	267.00	12.67	0.23
Lys	AAG	1360.00	64.55	0.93
Lys	AAA	108.00	5.13	0.07
Asn	AAT	127.00	6.03	0.13
Asn	AAC	878.00	41.67	0.87
Met	ATG	387.00	18.37	1.00
Ile	ATA	4.00	0.19	0.00
Ile	ATT	390.00	18.51	0.29
Ile	ATC	969.00	45.99	0.71
Thr	ACG	114.00	5.41	0.08
Thr	ACA	34.00	1.61	0.02

*Fig. 8A*

Thr	ACT	164.00	7.78	0.11
Thr	ACC	1127.00	53.49	0.78
Trp	TGG	243.00	11.53	1.00
End	TGA	1.00	0.05	0.01
Cys	TGT	20.00	0.95	0.08
Cys	TGC	220.00	10.44	0.92
End	TAG	12.00	0.57	0.17
End	TAA	58.00	2.75	0.82
Tyr	TAT	113.00	5.36	0.16
Tyr	TAC	574.00	27.25	0.84
Leu	TTG	210.00	9.97	0.12
Leu	TTA	9.00	0.43	0.01
Phe	TTT	62.00	2.94	0.09
Phe	TTC	635.00	30.14	0.91
Ser	TCG	195.00	9.26	0.17
Ser	TCA	29.00	1.38	0.02
Ser	TCT	103.00	4.89	0.09
Ser	TCC	558.00	26.49	0.48
Arg	CGG	7.00	0.33	0.01
Arg	CGA	25.00	1.19	0.03
Arg	CGT	281.00	13.34	0.34
Arg	CGC	465.00	22.07	0.55
Gln	CAG	703.00	33.37	0.91
Gln	CAA	66.00	3.13	0.09
His	CAT	88.00	4.18	0.22
His	CAC	312.00	14.81	0.78
Leu	CTG	1182.00	56.10	0.69
Leu	CTA	21.00	1.00	0.01
Leu	CTT	55.00	2.61	0.03
Leu	CTC	224.00	10.63	0.13
Pro	CCG	84.00	3.99	0.09
Pro	CCA	135.00	6.41	0.15
Pro	CCT	72.00	3.42	0.08
Pro	CCC	626.00	29.71	0.68

*Fig. 8B*

Codon usage for enteric bacterial (highly expressed) genes

AmAcid	Codon	Number	/1000	Fraction
Gly	GGG	13.00	1.89	0.02
Gly	GGA	3.00	0.44	0.00
Gly	GGU	365.00	52.99	0.59
Gly	GGC	238.00	34.55	0.38
Glu	GAG	108.00	15.68	0.22
Glu	GAA	394.00	57.20	0.78
Asp	GAU	149.00	21.63	0.33
Asp	GAC	298.00	43.26	0.67
Val	GUG	93.00	13.50	0.16
Val	GUA	146.00	21.20	0.26
Val	GUU	289.00	41.96	0.51
Val	GUC	38.00	5.52	0.07
Ala	GCG	161.00	23.37	0.26
Ala	GCA	173.00	25.12	0.28
Ala	GCU	212.00	30.78	0.35
Ala	GCC	62.00	9.00	0.10
Arg	AGG	1.00	0.15	0.00
Arg	AGA	0.00	0.00	0.00
Ser	AGU	9.00	1.31	0.03
Ser	AGC	71.00	10.31	0.20
Lys	AAG	111.00	16.11	0.26
Lys	AAA	320.00	46.46	0.74
Asn	AAU	19.00	2.76	0.06
Asn	AAC	274.00	39.78	0.94
Met	AUG	170.00	24.68	1.00
Ile	AUA	1.00	0.15	0.00
Ile	AUU	70.00	10.16	0.17
Ile	AUC	345.00	50.09	0.83
Thr	ACG	25.00	3.63	0.07
Thr	ACA	14.00	2.03	0.04

*Fig. 9A*

Thr	ACU	130.00	18.87	0.35
Thr	ACC	206.00	29.91	0.55
Trp	UGG	55.00	7.98	1.00
End	UGA	0.00	0.00	0.00
Cys	UGU	22.00	3.19	0.49
Cys	UGC	23.00	3.34	0.51
End	UAG	0.00	0.00	0.00
End	UAA	0.00	0.00	0.00
Tyr	UAU	51.00	7.40	0.24
Tyr	UAC	157.00	22.79	0.75
Leu	UUG	18.00	2.61	0.03
Leu	UUA	12.00	1.74	0.02
Phe	UUU	51.00	7.40	0.24
Phe	UUC	166.00	24.10	0.76
Ser	UCG	14.00	2.03	0.04
Ser	UCA	7.00	1.02	0.02
Ser	UCU	120.00	17.42	0.34
Ser	UCC	131.00	19.02	0.37
Arg	CGG	1.00	0.15	0.00
Arg	CGA	2.00	0.29	0.01
Arg	CGU	290.00	42.10	0.74
Arg	CGC	96.00	13.94	0.25
Gln	CAG	233.00	33.83	0.86
Gln	CAA	37.00	5.37	0.14
His	CAU	18.00	2.61	0.17
His	CAC	85.00	12.34	0.83
Leu	CUG	480.00	69.69	0.83
Leu	CUA	2.00	0.29	0.00
Leu	CUU	25.00	3.63	0.04
Leu	CUC	38.00	5.52	0.07
Pro	CCG	190.00	27.58	0.77
Pro	CCA	36.00	5.23	0.15
Pro	CCU	19.00	2.76	0.08
Pro	CCC	1.00	0.15	0.00

*Fig. 9B*

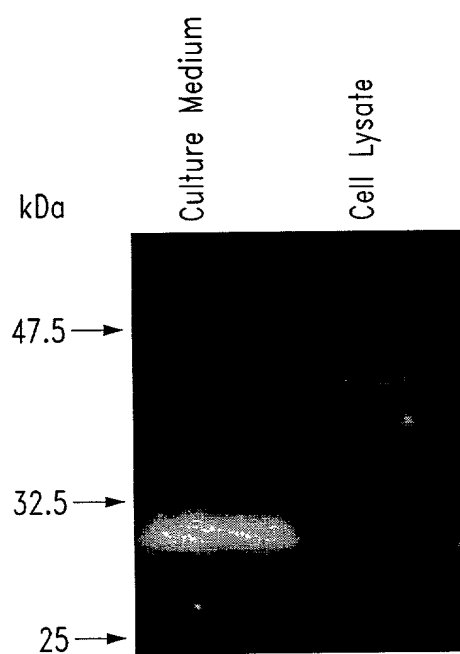
Chromosomal localization of genes of the FGF family in human

Gene	Localization	Gene	Localization
FGF-1	5q31.3-q33.2	FGF-12	3q29-qter
FGF-2	4q26	FGF-13	X
FGF-3	11q13	FGF-14	13
FGF-4	11q13.3	(FGF-15)	
FGF-5	4q21	FGF-16	-
FGF-6	12p13	FGF-17	8p21
FGF-7	15q13-q22	FGF-18	5
FGF-8	10q25-q26	FGF-19	11q13.1
FGF-9	13q11-q12	FGF-20	8p21.3-p22
FGF-10	5p12-p13	FGF-21	19q13.1-qter
FGF-11	17	FGF-22	19p13.3
		FGF-23 □	12p13

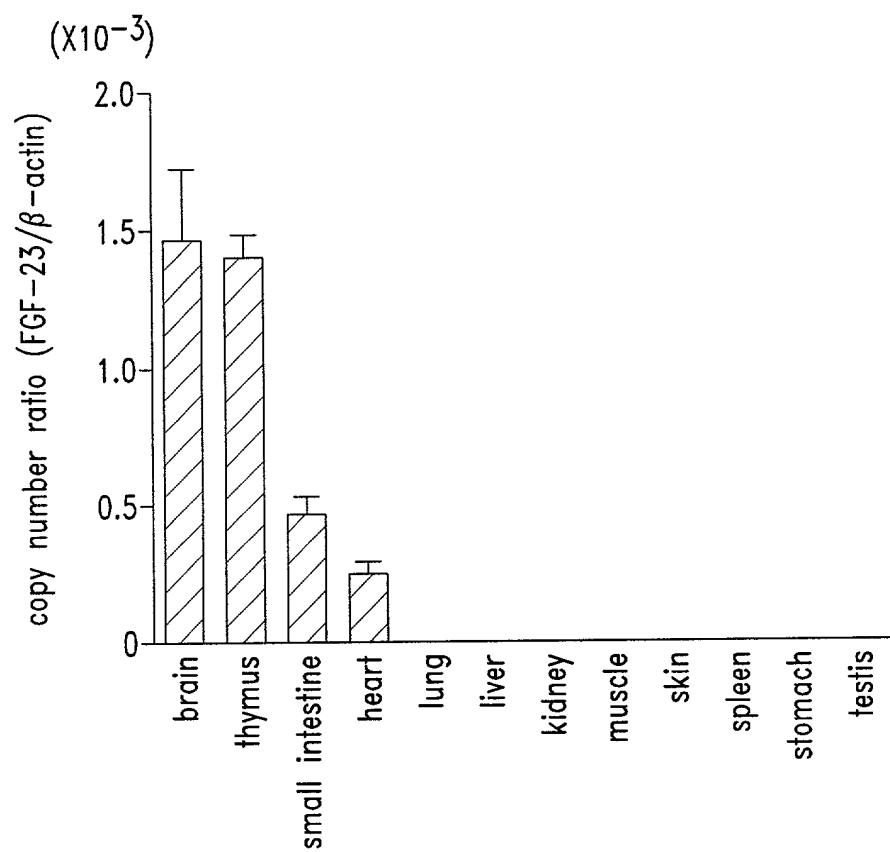
Human FGF-15 gene has not been identified. The localization of human FGF-16 gene has not been determined.

*Fig. 10*

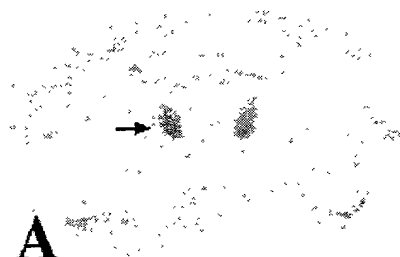




*Fig. 11*



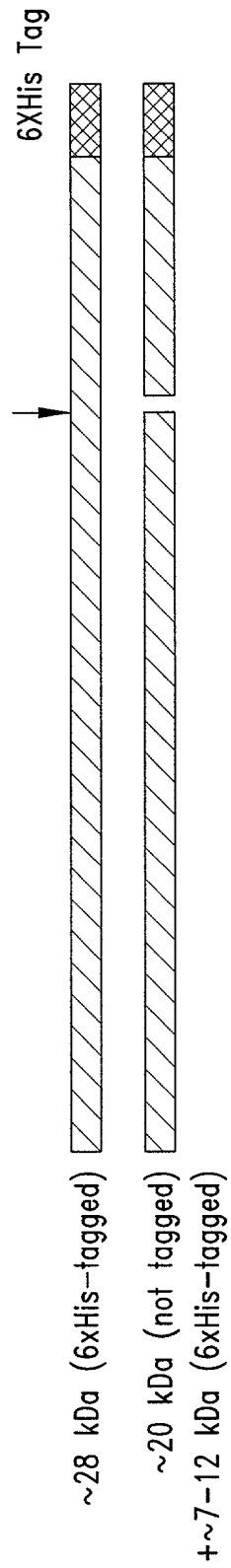
*Fig. 12*



*Fig. 13A*



*Fig. 13B*



*Fig. 14*

		11774 kDa			9713 kDa	7520 kDa	
	(213)	213	220	230	240	250	
FGF23	(141)	AKRAFL	PGMNP	PPYSQFLSR	NEIPLTH	NTPIPRRHTRSAEDDSER	
hFGF-1	(121)	NWFLVGL	KKNGS	CKRGP	-RTHYGQKAIL	FLPLPVSSD	-----
hFGF-10	(175)	QMYVAL	NGKG	APRRGQ	-KTRRKNTSAHFL	PMVHS	-----
hFGF-11	(170)	AWYLGL	DKEGQ	VMKGN	-RVKKTKAAAHFL	PKLLEVAMYQ	-----
hFGF-12	(172)	AWFLGL	NKEGQ	IMKGN	-RVKKTKPSSHFP	KPIEVCMYR	-----
hFGF-13	(168)	GWYLGL	NKEGE	IMKGN	-HVKKNKPAAHFL	PKPLKVAMYK	-----
hFGF-14	(170)	AWFLGL	NKEGQ	AMKGN	-RVKKTKPAAHFL	PKPLEVAMYR	-----
hFGF-15	(175)	AWFLGL	NKEGQ	AMKGN	-RVKKTKPAAHFL	PKPLEVAMYR	-----
hFGF-16	(160)	QYYVAL	NKDGSP	REGY	-RTKRHQKFTHFL	PRVPDPSKLP	-----
hFGF-17	(149)	-WMAFT	TRQGR	PROAS	-RSRQNRQEAHF	IKRLYQGQLPFPNHAEK	-
hFGF-18	(149)	-WYVGF	TKKGR	PRKGP	-KTRENQQDVHFM	KRYPKGQPEL	-----
hFGF-19	(141)	-LPVSL	SSAKQ	-RQLY	-KNRGFLPLSHFL	PMLPMVPEEP	-----E-
hFGF-2	(123)	-WYVAL	KRTGQY	KLGS	-KTGPGQKAIL	FLPMSAKS	-----
hFGF-21	(143)	-LPLHL	PGNKSP	HRDP	----APRGP	-ARFLPLPGLPPALP	-----
hFGF-3	(152)	LWYVSV	NGKGR	PRRGF	-KTRRTQKSSL	FLPRVLDHRDHEMVRQLQ	-
hFGF-4	(177)	-MFIAL	SKNGK	TKKGN	-RVSPTMKVTHFL	PRL	-----
hFGF-5 pLTR122	(187)	EWYVAL	NKRGK	AKRGCS	PRVKPQHISTHFL	PRFKQSEQPELSFTVTV	
hFGF-6	(179)	-TYIAL	SKYGR	VKRG	-KVSPIMTVTHFL	PRI	-----
hFGF-7	(162)	EMFVAL	NQKGI	PVRGK	-KTKKEQKTAHFL	PMAIT	-----
hFGF-8	(167)	-WMAFT	TRKGR	PRKGS	-KTRQHQREVHFM	KRLPRGHHTT	-----EQ-
hFGF-9	(161)	RYYVAL	NKDGT	PREGT	-RTKRHQKFTHFL	PRVPDPKVP	-----
hFGF-20	(164)	RYFVAL	NKDGT	PRDGA	-RSKRHQKFTHFL	PRVPDPERVP	-----
hFGF-22Nobu	(139)	-MFLAL	DRGGP	PRGG	-RTRRYHL	SAHFLPVLVS	-----
Consensus	(213)	WYVAL	K G PRKG	RTKK	AHFLPR	V	

*Fig. 15A*

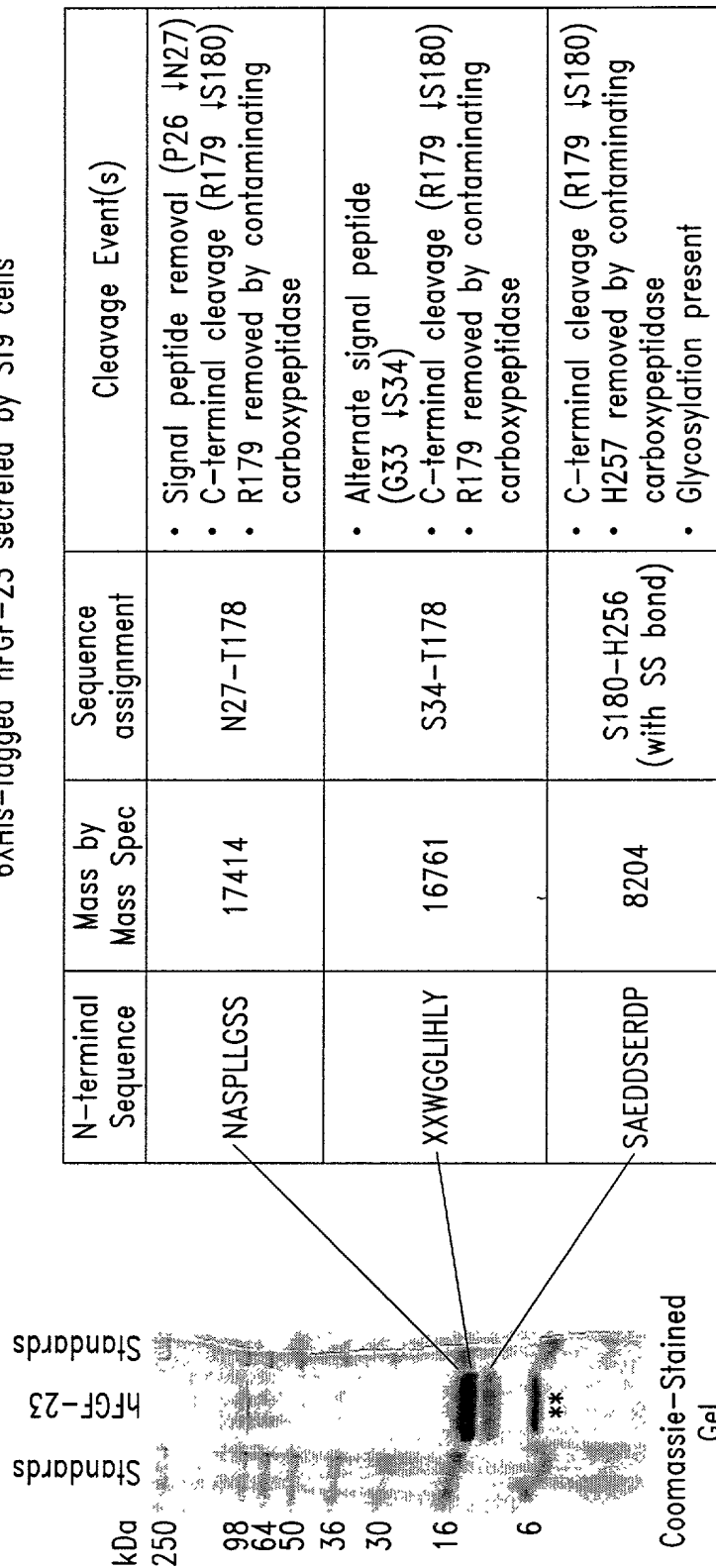
6630 kDa

260	270	280	290	300	310	323
DPLNVLKPRARMTAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFAKFI						
-----						
-----						
EPSLHSVPEAS-----P--SSPPAP-----						
EPSLHEIGE---KQGR-S--RKSSGTPTMGGKVVNQDST-----						
EPSLHDLTEFS-RSGSGTPTKRSVSGVLNNGKSMHNEST-----						
EPSLHDVGETVPKPGV-TPSKSTSASAIMNGGKPVNKSKT-----						
EPSLHDVGETVPKPGV-TPSKSTSASAIMNGGKPVNKSKT-----						
SMSRDLFHYR-----						
KQQFEFVGSAPTRRTKRTRR----PQPLT-----						
QKPFKYTTVTKRRIIRPTH----PA-----						
DLRGHLESDMFSSPLETDSMDPFGLVTGLEAVRSPSFEK-----						
-----						
EPPGILAPQPP-DVGSSDPLSMVGPSQGRSPSYAS-----						
SGLPRPPGKGVQPRRRRQKQSPDNLEPSHVQASRLGSQLEASAH-----						
-----						
PEKKKPPSPIKPKIPLSAPRKNTNSVKYRLKFRFG-----						
-----						
-----						
SLRFEFLNYPPFTRSLRGSQRTWAPEPR-----						
ELYKDILSQS-----						
ELYKDLLMYT-----						
-----						

*Fig. 15B*

FIG. 16

Cleavage of baculovirus-expressed  
 6XHis-tagged hFGF-23 secreted by Sf9 cells



\*\* aprotinin (added to preparation)

Fig. 16